



(5') 1 SDLEQERRAKEKLQEQQ  
18 SDLEQDRLAKEKLQEQQ  
35 SDLEQERLAKEKLQEQQ  
52 SDLEQERRAKEKLQEQQ  
69 SDLEQERRAKEKLQEQQ  
86 SDLEQDRLAKEKLQEQQ  
103 SDLEQERRAKEKLQEQQ  
120 SDLEQERKAKEKLQEQQ  
137 SDLEQERLAKEKLQEQQ  
154 SDLEQERRAKEKLQEQQ  
171 SDLEQERRAKEKLQEQQ  
188 SDLEQERRAKEKLQEQQ  
205 RDLEQ  
  
210 RKADTKKNLERKKEHGDILAEDLYGRLEIP  
240 AIELPSENERGYYPHQSSLPQDNRGNSRD  
270 SKEISIIIEKTNRESITTNVEGRRDIHKGHL  
300 EEKKGSGSIKPEQKEDKS 316 (3')

FIGURE 1

00000000-071001

(5') 1 AAAGCGATCTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 52 AAAGCGATTTAGAACAAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC  
 103 AAAGCGATTTAGAACAAAGAGAGACCTTGCTAAAGAAAAGTTGCAAGAACAAAC  
 154 AAAGCGATCTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 205 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 256 AAAGCGATTTAGAACAAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC  
 307 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 358 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 409 AAAGCGATTTAGAACAAAGAGAGACCTTGCTAAAGAAAAGTTGCAAGAACAAAC  
 460 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 511 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC  
 562 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC  
 613 AAAGAGATTTAGAACAA  
 630 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAGGAACATGGAGAT  
 681 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT  
 732 CCATCAGAAAATGAACGTGGATATTATATACACATCAATCTTTTACCT  
 783 CAGGACAAACAGAGGGAATAGTAGAGATCCAGGAAATATCTATAATAGAA  
 834 AAACCAAATAGAGAAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA  
 885 CATAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA  
 936 AAAGAAGATAAATCT 950 (3')

FIGURE 2

RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVKSVQQEQQ  
HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI  
ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE  
ESVAPSVVEESVAEMLKER

### FIGURE 3

FIGURE 3

FOOT 20- E9600660

5' GAA TTC CGT GAT GAA CTT TTT AAT GAA TTA TTA AAT AGT GTA GAT  
GTT AAT GGA GAA GTA AAA GAA AAT ATT TTG GAG GAA AGT CAA GTT AAT  
GAG GAT ATT TTT AAT AGT TTA GTA AAA AGT GTT CAA CAA GAA CAA CAA  
CAC AAT GTT GAA GAA AA AGT TGA AGA AAG TGT AGA AGA AA ATG ACG  
AAG AAA GTG TAG AAG AAA ATG TAG AAG AAA ATG TAG AAG AAA ATG  
ACG ACG GAA GTG TAG CCA GTG TTG AAG AAA ATA TAG CTT CAA GTG  
TTG ATG AAA GTA TAG ATT CAA GTA TTG AAG AAA ATG TAG CTC CAA CTG  
TTG AAG AAA TCG TAG CTC CAA CTG TTG AAG AAA TTG TAG CTC CAA GTG  
TTG TAG AAA AGT GTG CTC CAA GTG TTG AAG AAA GTG TAG CTC CAA GTG  
TTG AAG AAA GTG TAG CTG AAA TGT TGA AGG AAA GGA ATT C 3'

FIGURE 4

FOOT 20 29600660

NSRDSKEISIIIEKTNRESITTTNVEGRRDIHK

LSA-TER

DELFNELLNSVDVNGEVKENILEESQ  
LEESQVNDDDIFSNLSLVKSVQEQQHNV  
VEKCAPSVEESVAPSVVEESVAEMLKER

729S-NRI  
729S-NRII  
729S-Rep

FIGURE 5

NUCLEOTIDE SEQUENCE OF THE LSA GENE  
5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

33 ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG  
84 ATATTTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA  
135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA  
186 GGAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAAAC  
237 AAAAATAATGAAAATAATAAATTTTTTCGATAAGGATAAAGAGTTAACGATGT  
288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAGTCTTTTAAGAAATCT  
339 TGGTGTTCAGAGAATATATTCCTTAAAGAAAATAAATTAATAAAGGAAGGG  
390 AAATTAATTGAACACATAATAAATGATGATGACGATAAAAAAAAAATATATTA  
441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAAGCA

(CODING 5' END, repetitive)

492 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGT  
543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACTT  
594 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACGT  
645 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACTT  
696 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACGT  
747 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACGT  
798 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACTT  
849 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTGAGAACAAGATAGACTT  
900 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGAACAAGAGAGACGT  
951 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTGAGA 988

FIGURE 6

DNA sequence · 956 b.p. ATGAACATATT ... AAGGATTTAGA linear

[illegible]

FIGURE 7A

361 /	121	391 /	131
GGG AAA	TTA ATT	ATA AAT	GAT GAT
gly lys	ile glu	ile ile	asp asp
421 /	141	451 /	151
CAA GAC	GAA AAC	GAT GAT	GAA CTT
gln asp	glu arg	glu asp	leu glu
481 /	161	511 /	171
CAA CAA	AGC GAT	TCA GAA	GAG AGA
gln gln	ser asp	glu gln	arg arg
541 /	181	571 /	191
GAT TTA	GAA CAA	GCT GCT	AAA AGA
asp leu	glu gln	ala lys	glu glu
601 /	201	631 /	211
CAA GAG	AGA CGT	GCT AAA	TTG CAA
gln glu	arg ala	lys glu	gln asp
661 /	221	691 /	231
CTT GCT	AAA GAA	AAG TTA	GAA CAA
leu ala	lys glu	asp leu	gln glu
721 /	241	751 /	251
GAA AAG	TTG CAA	AGC GAT	TTA GAA
glu lys	leu gln	ser asp	leu glu

FIGURE 7B



FOOT 20-29000000

781 /	261	811 /	271
CAA GAA CAA	CAA AGC GAT TTA GAA CAA GAG	AGA CTT GCT AAA GAA AAG	TTA CAA GAG CAG
gln glu gln	gln ser asp leu glu gln	arg leu ala lys glu lys	leu gln glu gln
841 /	281	871 /	291
CAA AGC GAT	TTA GAA CAA GAT AGA CTT GCT	AAA GAA AAG TTG CAA GAA CAA	AGC GAT
gln ser asp	leu glu gln asp arg leu ala	lys leu gln glu gln	gln ser asp
901 /	301	931 /	311
TTA GAA CAA	GAG AGA CGT GCT AAA GAA AGG	TTG CAA GAA CAA CAA	AGC GAT TTA
leu glu gln	glu arg arg ala lys glu arg	leu gln glu gln	ser asp leu

FIGURE 7C

NUCLEOTIDE SEQUENCE OF THE LSA GENE  
3' END

(CODING 3' END, REPETITIVE)

1 CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT  
37 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT  
88 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT  
139 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT  
190 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
241 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT  
292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT  
343 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT  
445 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
496 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
598 GCTAAAGAAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

(CODING 3' END, UNIQUE)

640 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT  
691 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT  
742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT  
793 CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA  
844 AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA  
895 CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA  
946 AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT  
997 ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT  
1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT  
1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA  
1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT  
1201 TAGATGATTTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG  
1252 AAAAAATAAAAAAAGGAAAGAAATATGAAAAACAAAGGATAATAATTTTA  
1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAAAAAATATAAAAATG  
1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTGTTTCATA  
1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG  
1456 ATATAACTAAATATTTTATGAACTATAA (stop)

(NON-CODING 3' END)

1485 AAGGTTATATATTT 1498

FIGURE 8

LSA.3'.ALL -> 1-phase Translation

DNA sequence 1496 b.p. CAAGAACAACAA ... GGTATATATTT linear

1 / 1	31 / 11	
CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA		
gln glu gln gln ser asp leu glu gln glu arg ala lys glu lys leu gln glu gln		
61 / 21	91 / 31	
CAA AGC GAT TTA GAA CAA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT		
gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln ser asp		
121 / 41	151 / 51	
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA		
leu glu gln glu arg leu ala lys glu lys leu gln glu gln ser asp leu glu gln		
181 / 61	211 / 71	
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAG AGA CGT		
glu arg arg ala lys glu lys leu gln glu gln ser asp leu glu gln arg arg		
241 / 81	271 / 91	
GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA		
ala lys glu lys leu gln glu gln ser asp leu glu gln asp arg leu ala lys glu		
301 / 101	331 / 111	
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA		
lys leu gln glu gln ser asp leu glu gln glu arg ala lys glu lys leu gln		

FIGURE 9A

361	/	121		391	/	131	
GAA	CAA	AGC	GAT	TTA	GAA	GAG	AGA
glu	gln	ser	asp	leu	glu	gln	arg
421	/	141		451	/	151	
AGC	GAT	TTA	GAA	AGC	CTT	GCT	AAA
ser	asp	leu	glu	arg	leu	ala	lys
481	/	161		511	/	171	
GAA	CAA	AGC	GAT	TTA	GAA	GAG	AGA
glu	gln	arg	arg	ala	lys	gln	lys
541	/	181		571	/	191	
AGA	CGT	GCT	AAA	GAA	GAA	GAG	TTG
arg	arg	ala	lys	glu	lys	lys	leu
601	/	201		631	/	211	
AAA	GAA	AGC	GAT	TTA	GAA	GAG	TTA
lys	glu	lys	leu	gln	gln	gln	lys
661	/	221		691	/	231	
AAT	TTA	GAA	AGC	GAT	TTA	GAG	GAT
asn	leu	glu	arg	lys	his	gly	asp
721	/	241		751	/	251	
GAA	ATA	CCA	GCT	ATA	GAA	CTT	GAA
glu	ile	pro	ala	ile	glu	leu	asn
781	/	261		811	/	271	
TCT	TCT	TTA	CCT	CAG	GAC	AAC	AGA
ser	ser	leu	pro	gln	asp	asn	arg

FIGURE 9B

841 / 281	871 / 291	
GAA AAA ACA AAT AGA GAA TCT ATT ACA	ACA thr thr	GGA GGA AGG GAT ATA CAT AAA
glu lys thr asn arg glu ser ile thr		glu gly arg asp ile his lys
901 / 301	931 / 311	
GGA CAT CTT GAA AAG AAA GAT GGT TCA ATA AAA CCA GAA CAA GAT AAA TCT		
gly his leu glu lys lys asp gly ser ile lys pro glu gln lys glu asp lys ser		
961 / 321	991 / 331	
GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA GTA AAT ATT TCT GAT GTT AAT GAT TTT CAA		
ala asp ile gln asn his thr leu glu thr val asn ile ser asp val asn phe gln		
1021 / 341	1051 / 351	
ATA AGT AAG TAT GAG GAT GAT GCT GAA TAT GAC GAT TCA TTA ATA GAT GAA GAA		
ile ser lys tyr glu asp glu ile ser ala glu tyr asp asp leu ile asp glu glu		
1081 / 361	1111 / 371	
GAA GAT GAT GAA GAC TTA GAC GAA TTT AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT		
glu asp asp glu asp leu asp glu phe lys pro ile val gln tyr asp asn phe gln asp		
1141 / 381	1171 / 391	
GAA GAA AAC ATA GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA		
glu glu asn ile gly ile tyr lys glu leu glu asp leu ile glu lys asn glu asn leu		
1201 / 401	1231 / 411	
GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA GAA GAA TTA TCT GAA GAA AAA ATA AAA		
asp asp leu asp glu gly ile glu lys ser ser glu glu leu ser glu glu lys ile lys		

FIGURE 9C

FOOT 20" E9600660

1261 / 421	1291 / 431
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG	
lys gly lys lys tyr glu lys thr lys asp asn asn phe lys pro asn asp lys ser leu	
1321 / 441	1351 / 451
TAT GAT GAG CAT ATT AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA	
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys	
1381 / 461	1411 / 471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT	
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp	
1441 / 481	1471 / 491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT	
glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr	

FIGURE 9D

LSN.3'STOP -> 1-phase Translation

DNA sequence 1482 b.p. CAAGAACAACAA ... ATGAAACTATAA linear

1 / 1	31 / 11	
CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA GAA		
gln glu gln gln ser asp leu glu gln glu arg ala lys glu lys leu gln glu gln		
61 / 21	91 / 31	
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT		
gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln ser asp		
121 / 41	151 / 51	
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA		
leu glu gln glu arg leu ala lys glu lys leu gln glu gln ser asp leu glu gln		
181 / 61	211 / 71	
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT		
glu arg arg ala lys glu lys leu gln glu gln ser asp leu glu gln arg arg		
241 / 81	271 / 91	
GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA		
ala lys glu lys leu gln glu gln ser asp leu glu gln asp arg leu ala lys glu		
301 / 101	331 / 111	
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA		
lys leu gln glu gln ser asp leu glu gln glu arg ala lys glu lys leu gln		

FIGURE 10A

FIGURE 10B

361 / 121	GAA CAA CAA	AGC GAT TTA	GAA GAG	AGA CGT GCT	AAA GAA AAG	TTG CAA GAA	CAA CAA CAA	CAA CAA CAA
421 / 141	glu gln gln	ser asp leu	glu gln gln	arg arg ala	lys glu lys	leu glu gln	leu glu gln	gln gln gln
481 / 161	AGC GAT TTA	GAA CAA GAG	AGA CTT GCT	AAA GAA AAG	TTG CAA GAA	CAA CAA CAA	CAA CAA CAA	CAA CAA CAA
541 / 181	ser asp leu	glu gln gln	glu arg leu	ala ala ala	lys glu lys	leu glu gln	leu glu gln	asp asp leu
601 / 201	GAA CAA GAG	AGA CGT GCT	AAA GAA AAG	TTG CAA GAA	CAA CAA CAA	CAA CAA CAA	CAA CAA CAA	CAA CAA CAA
661 / 221	glu gln gln	arg arg ala	lys glu lys	leu glu gln	lys glu gln	ser asp leu	leu glu gln	glu gln gln
721 / 241	AGA CGT GCT	AAA GAA AAG	TTG CAA GAA	CAA CAA CAA	CAA CAA CAA	CAA CAA CAA	CAA CAA CAA	CAA CAA CAA
781 / 261	arg arg ala	lys glu lys	leu glu gln	leu glu gln	ser asp leu	leu glu gln	leu glu gln	ala arg ala
841 / 281	AAA GAA AAG	TTG CAA GAG	CAG CAA AGA	GAT TTA GAA	AGG AAG AAG	GCT GAT GAT	ACG AAA AAA	AAA AAA AAA
901 / 301	lys glu lys	leu gln gln	gln gln gln	asp leu gln	arg arg lys	ala ala ala	thr thr thr	lys lys lys
961 / 321	AAT TTA GAA	AGA AAA AAG	AAA GAA AAG	TTA GCA GAG	GAT TTA GCA	GAT TTA GCA	GGT CGT TTA	TTA TTA TTA
1021 / 341	asn leu glu	lys lys lys	glu his his	asp ile leu	ala ala ala	asp leu leu	tyr gly arg	leu leu leu
1081 / 361	721 / 241	GAA ATA CCA	GCT ATA GAA	CTT CCA TCA	GAA AAT GAA	CGT GGA TAT	TAT ATA CCA	CAT CAA CAA
1141 / 381	glu ile pro	ala ala ala	ile ile ile	leu pro pro	glu asn glu	arg gly tyr	ile pro his	gln gln gln
1201 / 401	781 / 261	TCT TCT TTA	CCT CAG GAC	AAC AGA GGG	AAT AGT AGA	GAT TCC AAG	GAA ATA TCT	ATA ATA ATA
1261 / 421	ser ser leu	pro pro pro	gln asp asp	asn arg arg	ser arg ser	lys lys lys	glu ile ser	ile ile ile

FIGURE 10B



FIGURE 10C

TTTTCCCGGGGGGG

1321 / 441	1351 / 451
TAT GAT GAG CAT ATT AAA	AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys	lys tyr lys asn asp lys gln val asn lys glu lys glu lys
1381 / 461	1411 / 471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GAC AAT GAA ATT TTA CAG ATC GTG GAT	
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp	
1441 / 481	1471 / 491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT	
glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr	

FIGURE 10D